RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/509,954_

Source: _PCT/10_

Date Processed by STIC: _1/9/06_

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 01/09/2006
PATENT APPLICATION: US/10/509,954   TIME: 11:22:12

Input Set : A:\32436ASEQLIST.TXT
Output Set: N:\CRF4\01092006\J509954.raw

```
 4 <110> APPLICANT: Barclay, Jane
 5         Buxton, Francis Paul
 6         Ganju, Pamposh
 7         Natt, Francois Jean-Charles
 8         Song, Chuanzheng
 9         Weiler, Jan
10         Wishart, William Leonard
12 <120> TITLE OF INVENTION: Use of MOB-5 in Pain
15 <130> FILE REFERENCE: PN/4-32436A
17 <140> CURRENT APPLICATION NUMBER: 10/509,954
18 <141> CURRENT FILING DATE: 2004-10-04
20 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03469
21 <151> PRIOR FILING DATE: 2003-04-02
23 <150> PRIOR APPLICATION NUMBER: 60/369,893
24 <151> PRIOR FILING DATE: 2002-04-03
26 <160> NUMBER OF SEQ ID NOS: 20
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 29
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Primer Sequences for Rat MOB-5 gene
38 <400> SEQUENCE: 1
39 atgcagacaa gcttgagaca acagattct                              29
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 27
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Primer Sequences for Rat MOB-5 gene
49 <400> SEQUENCE: 2
50 tcagagctgg tagaaattct gcatcca                                27
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 393
54 <212> TYPE: DNA
55 <213> ORGANISM: Rattus
57 <220> FEATURE:
58 <221> NAME/KEY: prim_transcript
59 <222> LOCATION: (28)...(48)
60 <223> OTHER INFORMATION: Gene Specific Primer Sequence designed from Rat
61         MOB-5 gene
63 <221> NAME/KEY: prim_transcript
```

```
  64 <222> LOCATION: (175)...(198)
  65 <223> OTHER INFORMATION: Gene Specific Primer Sequence designed from Rat
  66      MOB-5 gene
W--> 68 <400> 3
  69 cttgattgcc aatccggata acttcctcct ttgttctccg tgccatttca aggcattgtt 60
  70 catatccctg ttgtcctcag ggcacttcag acccttggcc atggacccct gtcgttggct 120
  71 caggcttttc ttcagacctc actctttagt ccaaacgaca gccatggaca gcacctttgg 180
  72 atgctccgac tgacccacaa cgtggatttg catatttatt acagccctat ttaactaatg 240
  73 tcactgtttc ggtagaaacc ggtatttatt tgtgagactg gacgttccat gaaagcatca 300
  74 tgccccgtgt ttgcacctta cttcctgtga gctggctcac catgggggca gtagatggtt 360
  75 gctcagtaaa tatttaaaat ggaaaaaaaa aaa                              393
  77 <210> SEQ ID NO: 4
  78 <211> LENGTH: 21
  79 <212> TYPE: DNA
  80 <213> ORGANISM: Artificial Sequence
  82 <220> FEATURE:
  83 <223> OTHER INFORMATION: RT-PCR Primer region for rat MOB-5 gene
  85 <400> SEQUENCE: 4
  86 cctttgttct ccgtgccatt t                                          21
  88 <210> SEQ ID NO: 5
  89 <211> LENGTH: 23
  90 <212> TYPE: DNA
  91 <213> ORGANISM: Artificial Sequence
  93 <220> FEATURE:
  94 <223> OTHER INFORMATION: RT-PCR Primer region for rat MOB-5 geneMOB-5 gene
  96 <400> SEQUENCE: 5
  97 ctttggatgc tccgactgac cca                                        23
  99 <210> SEQ ID NO: 6
 100 <211> LENGTH: 183
 101 <212> TYPE: PRT
 102 <213> ORGANISM: Rattus
 104 <220> FEATURE:
 105 <221> NAME/KEY: PEPTIDE
 106 <222> LOCATION: (1)...(183)
 107 <223> OTHER INFORMATION: Amino Acid sequence corresponding to the Open
 108      Reading Frame region deduced from MOB-5 cDNAs
 109      Cloned from Rattus Dorsal Root Ganglia
 111 <400> SEQUENCE: 6
 112 Met Gln Thr Ser Leu Arg Gln Gln Ile Leu Pro Gly Leu Ser Leu Ile
 113 1               5                   10                  15
 114 Leu Leu Val Leu Ser Gln Val Pro Glu Leu Gln Gly Gln Glu Phe Arg
 115             20                  25                  30
 116 Phe Gly Pro Cys Gln Val Thr Gly Val Val Leu Pro Glu Leu Trp Glu
 117         35                  40                  45
 118 Ala Phe Trp Thr Val Lys Asn Thr Val Lys Thr Gln Asp Glu Leu Thr
 119     50                  55                  60
 120 Ser Val Arg Leu Leu Lys Pro Gln Val Leu Gln Asn Val Ser Asp Ala
 121 65                  70                  75                  80
 122 Glu Ser Cys Tyr Leu Ala His Ser Leu Leu Lys Phe Tyr Leu Asn Thr
```

```
123                     85              90              95
124 Val Phe Lys Asn Tyr His Ser Glu Ile Val Lys Phe Lys Val Leu Lys
125             100             105             110
126 Ser Phe Ser Thr Leu Ala Asn Asn Phe Leu Val Ile Met Ser Lys Leu
127         115             120             125
128 Gln Pro Ser Lys Asp Asn Ala Met Leu Pro Ile Ser Asp Ser Ala Arg
129     130             135             140
130 Arg Arg Phe Leu Leu Phe His Arg Thr Phe Lys Gln Leu Asp Ile Glu
131 145             150             155             160
132 Val Ala Leu Ala Lys Ala Phe Gly Glu Val Asp Ile Leu Leu Ala Trp
133             165             170             175
134 Met Gln Asn Phe Tyr Gln Leu
135             180
138 <210> SEQ ID NO: 7
139 <211> LENGTH: 18
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Antisense Oligonucleotide
```
W--> 146 `<221> NAME/KEY: modified_base`
```
147 <222> LOCATION: 1-5, 14-18
148 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl)
```
W--> 150 `<221> modified_base`
```
151 <222> LOCATION: 6-13
152 <223> OTHER INFORMATION: modified with a phosphorothioate group
```
W--> 154 `<221> modified_base`
```
155 <222> LOCATION: 2,5,16
156 <223> OTHER INFORMATION: m5c
```
W--> 158 `<400> 7`
```
159 tcagcaggct gtgggcaa                                          18
161 <210> SEQ ID NO: 8
162 <211> LENGTH: 18
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Antisense Oligonucleotide
```
W--> 169 `<221> NAME/KEY: modified_base`
```
170 <222> LOCATION: 1-5, 14-18
171 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
```
W--> 173 `<221> modified_base`
```
174 <222> LOCATION: 6-13
175 <223> OTHER INFORMATION: modified with phosphorothioate group
```
W--> 177 `<221> modified_base`
```
178 <222> LOCATION: 2-3, 16
179 <223> OTHER INFORMATION: m5c
```
W--> 181 `<400> 8`
```
182 tccgaaggcg gtgtgcaa                                          18
184 <210> SEQ ID NO: 9
185 <211> LENGTH: 18
```

RAW SEQUENCE LISTING   DATE: 01/09/2006
PATENT APPLICATION: US/10/509,954   TIME: 11:22:12

Input Set : **A:\32436ASEQLIST.TXT**
Output Set: **N:\CRF4\01092006\J509954.raw**

```
      186 <212> TYPE: DNA
      187 <213> ORGANISM: Artificial Sequence
      189 <220> FEATURE:
      190 <223> OTHER INFORMATION: Antisense oligonucleotide
W-->  192 <221> NAME/KEY: modified_base
      193 <222> LOCATION: 1-5, 14-18
      194 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W-->  196 <221> modified_base
      197 <222> LOCATION: 2,5, 16
      198 <223> OTHER INFORMATION: m5c
W-->  200 <400> 9
      201 tcagcaggct gtgggcaa                                              18
      203 <210> SEQ ID NO: 10
      204 <211> LENGTH: 18
      205 <212> TYPE: DNA
      206 <213> ORGANISM: Artificial Sequence
      208 <220> FEATURE:
      209 <223> OTHER INFORMATION: Antisense oligonucleotide
W-->  211 <221> NAME/KEY: modified_base
      212 <222> LOCATION: 1-5, 14-18
      213 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W-->  215 <221> modified_base
      216 <222> LOCATION: 2,3, 16
      217 <223> OTHER INFORMATION: m5c
W-->  219 <400> 10
      220 tccgaaggcg gtgtgcaa                                              18
      222 <210> SEQ ID NO: 11
      223 <211> LENGTH: 549
      224 <212> TYPE: DNA
      225 <213> ORGANISM: Rattus
      227 <220> FEATURE:
      228 <221> NAME/KEY: gene
      229 <222> LOCATION: (1)...(549)
      230 <223> OTHER INFORMATION: Rat MOB-5 cDNA
      232 <400> SEQUENCE: 11
      233 atgcagacaa gcttgagaca acagattctc cccggcctga gcctaatcct tctcgttttg 60
      234 agccaagtac cagagcttca gggtcaagag ttccgatttg ggccttgcca agtgaccggg 120
      235 gtggttctcc cagaactgtg ggaggccttc tggactgtga agaacactgt gaaaactcag 180
      236 gacgagctca caagtgtccg gctgttgaaa ccacaggttc tgcagaatgt ctcggatgcc 240
      237 gagagctgtt accttgccca cagcctgctg aagttctact tgaacactgt tttcaaaaac 300
      238 tatcacagcg aaatagtcaa attcaaggtc ttgaagtcat tctccactct ggccaacaac 360
      239 tttttagtca tcatgtccaa actgcagcct agtaaggaca atgccatgct tcccattagt 420
      240 gacagtgcac gccggcgttt tttgctgttc cacagaacat tcaaacagtt ggacatagaa 480
      241 gtggctttgg cgaaagcctt tggggaagtg gacattctcc tggcctggat gcagaatttc 540
      242 taccagctc                                                        549
      244 <210> SEQ ID NO: 12
      245 <211> LENGTH: 21
      246 <212> TYPE: DNA
      247 <213> ORGANISM: Artificial Sequence
```

RAW SEQUENCE LISTING   DATE: 01/09/2006
PATENT APPLICATION: US/10/509,954   TIME: 11:22:12

Input Set : A:\32436ASEQLIST.TXT
Output Set: N:\CRF4\01092006\J509954.raw

```
      249 <220> FEATURE:
      250 <223> OTHER INFORMATION: Antisense Oligoribonucleotides sequence to rat
      251       MOB-5 gene
W--> 253 <221> NAME/KEY: modified_base
      254 <222> LOCATION: 1-18
      255 <223> OTHER INFORMATION: phosphodiester internucleotide linkage
W--> 257 <221> modified_base
      258 <222> LOCATION: 19-21
      259 <223> OTHER INFORMATION: deoxyribonucleoside internucleotide linkage
W--> 261 <400> 12
      262 uucagcaggc uguggggcaag g                                    21
      264 <210> SEQ ID NO: 13
      265 <211> LENGTH: 21
      266 <212> TYPE: DNA
      267 <213> ORGANISM: Artificial Sequence
      269 <220> FEATURE:
      270 <223> OTHER INFORMATION: Sense Oligoribonucleotides sequence to rat MOB-5
      271       gene
W--> 273 <221> NAME/KEY: modified_base
      274 <222> LOCATION: 1-18
      275 <223> OTHER INFORMATION: phosphodiester internucleotide linnkage
W--> 277 <221> modified_base
      278 <222> LOCATION: 19-21
      279 <223> OTHER INFORMATION: deoxyribobnucleoside internucleotide linkagechm5u
W--> 281 <400> 13
      282 uugcccacag ccugcugaat t                                     21
      284 <210> SEQ ID NO: 14
      285 <211> LENGTH: 21
      286 <212> TYPE: DNA
      287 <213> ORGANISM: Artificial Sequence
      289 <220> FEATURE:
      290 <223> OTHER INFORMATION: Mismatch Antisense Oligoribonucleotides to rat
      291       MOB-5 gene
W--> 293 <221> NAME/KEY: modified_base
      294 <222> LOCATION: 1-18
      295 <223> OTHER INFORMATION: phosphodiester internucleotide linkages
W--> 297 <221> modified_base
      298 <222> LOCATION: 19-21
      299 <223> OTHER INFORMATION: deoxyribose internucleotide linages
W--> 301 <400> 14
      302 uuccgaaggc ggugugcaag g                                     21
      304 <210> SEQ ID NO: 15
      305 <211> LENGTH: 21
      306 <212> TYPE: DNA
      307 <213> ORGANISM: Artificial Sequence
      309 <220> FEATURE:
      310 <223> OTHER INFORMATION: Mismatch Sense oligoribonucleotides to rat MOB-5
      311       gene
W--> 313 <221> NAME/KEY: modified_base
```

VERIFICATION SUMMARY   DATE: 01/09/2006
PATENT APPLICATION: **US/10/509,954**   TIME: 11:22:13

Input Set : **A:\32436ASEQLIST.TXT**
Output Set: **N:\CRF4\01092006\J509954.raw**

```
L:68  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:146 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:150 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:154 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:169 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:192 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:211 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:215 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:219 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:253 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:261 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:273 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:281 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:293 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:313 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:317 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:321 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:333 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:341 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:353 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:361 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:373 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:381 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:393 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:401 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:413 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
```